1: Appl Microbiol Biotechnol. 1993 Jan;38(4):493-501. Related Articles, Links

Cloning and molecular analysis of the poly(3-hydroxybutyric acid) biosynthetic genes of Thiocystis violacea.

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From a genomic library of Thiocystis violaceae strain 2311 in lambda L47, two adjacent EcoRI restriction fragments of 5361 base pairs (bp) and of 1978 bp were cloned. The 5361-bp EcoRI restriction fragment hybridized with a DNA fragment harbouring the Alcaligenes eutrophus poly(3-hydroxyalkanoate) (PHA) synthase operon (phbCAB) and restored the ability to synthesize and accumulate PHA in PHA-negative mutants derived from A. eutrophus. The nucleotide sequence analysis of both fragments revealed five open-reading frames (ORFs); at least three of them are probably relevant for PHA biosynthesis. The amino acid sequences of the putative proteins deduced from these genes indicate that they encode a beta-ketothiolase [phbATv, relative molecular mass (M(r)) 40850], which exhibited 87.3% amino acid identity with the beta-ketothiolase from Chromatium vinosum. The amino acid sequences of the putative proteins deduced from ORF2Tv (M(r) 41450) and phbCTv (M(r) 39550), which were located upstream of and antilinear to phbATv, exhibited 74.7% and 87.6% amino acid identity, respectively, with the corresponding gene products of C. vinosum. Downstream of and antilinear to phbCTv was located ORF5, which encodes for a protein of high relative molecular mass (M(r) 76428) of unknown function. With respect to the divergent organisation of ORF2Tv and phbCTv on one side and of phbATv on the other side and from the homologies of the putative gene products, this region of the T. violaceae genome resembled very much the corresponding region of C. vinosum, which was identified recently.

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